REMARKS

Firstly, claims 23-31 have been rewritten to recite the appropriate SEQ ID NOS for the elected sequences.

References to web-based hyperlinks have been deleted from the specification.

Rejection of the Claims Under 35 U.S.C. § 112, first paragraph

The claims stand rejected under 35 U.S.C. 112, first paragraph for allegedly lacking written description. Applicants respectfully traverse.

The pending claims have been rewritten to remove the term "partial". Also, claims 24 and 26 have been rewritten to include an associated functional activity. One of ordinary skill in the art, using conventional techniques in modern molecular biology, would be able to construct polypeptides having sequences which are 80% or 90% homologous to the polypeptide of SEQ ID NO:38 and possess the associated function identified as a human mRNA putatively prenylated protein, as described for the encoding SEQ ID NO:16. See e.g., the specification at page 55. Also, review of the expression data collected in a Northern blot analysis for SEQ ID NO:16 clearly indicates an expression of this nucleic acid in tumorous ovarian and breast tissue compared to normal ovarian and breast tissue expression (see specification at page 33). This correlation is not observed in the other tissue types. One of ordinary skill in the art, using conventional techniques or assays would be able to ascertain that the polypeptides having 80 or 90% homology have the associated functional activity. The rejection of the claims under §112, first paragraph is improper and should be withdrawn.

Rejection of the Claims Under 35 U.S.C. §112, second paragraph

Claims 27-31 stand rejected under 112, first paragraph for being in improper format for method claims. The claims have been rewritten in a format consistent with US practice for method claims. The claims have not been amended for any purpose related to patentability. The rejection of the claims is now moot and should be withdrawn.

Prior Art Rejection

Claims 23-26 stand rejected for allegedly being anticipated by Accession Number Q00833 (*Mol. Gen. Genetic.* Vol. 249, 1955). Applicants respectfully traverse.

Claim 23 has been rewritten to delete the term "partial" sequence. Accession Number Q00833 discloses a amino acid sequence which shows only 29 amino acid matches with the same amino acids of the polypeptide of SEQ ID NO:38 which is 144 amino acids long. This corresponds to about a 20 % homology. Therefore, the instant claims, including claims 24 and 26 which require 80% and 90% homology with SEQ ID NO:38, are clearly not anticipated by this prior art sequence. Rejection of the claims under 102(b) is clearly improper and should be withdrawn.

In view of the above remarks, favorable consideration is courteously requested. However, if there is any remaining issue(s) which can be expeditiously resolved by a telephone conference, the Examiner is courteously requested to telephone the undersigned at the number indicated below.

The Commissioner is hereby authorized to charge any fees associated with this response or credit any overpayment to Deposit Account No. 13-3402.

Attached hereto is a marked-up version of the changes made to the claims by the current amendment. The attached pages are captioned "Version With Markings to Show Changes Made".

Respectfully submitted,

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Version With Markings to Show Changes Made

IN THE CLAIMS

Please amend the claims as follows:

23. (Amended) An isolated polypeptide ~~Polypeptide partial sequences according to sequences Seq ID Nos. Seq. 32-51 and Seq. ID Nos. 53-55~~ comprising SEQ ID NO:38.

24. (Amended) An isolated polypeptide ~~Polypeptide partial sequences according claim 23, with~~ having at least 80% homology to ~~these sequences~~ SEQ ID NO: 38 according to claim 23 and wherein said polypeptide is a human mRNA putatively prenylated protein.

25. (Amended) A polypeptide ~~that is known~~ from a phage display ~~and~~ that can bind to the polypeptide ~~partial sequences~~ according to claim 23.

26. (Amended) ~~Polypeptide partial sequences~~ An isolated polypeptide having at least 90% homology to SEQ ID NO:38 according to claim 23~~, with at least 90% homology to these sequences~~ and wherein said polypeptide is a human mRNA putatively prenylated protein .

27. (Amended) ~~Use of polypeptide partial sequences according to sequences Seq. ID Nos. 32 to 51 and Seq. ID Nos. 53-55 as tools~~ A method for finding an active ~~ingredients~~ ingredient against hysteromyoma comprising measuring the binding of said ingredient to the isolated polypeptide sequence comprising SEQ ID NO:38 according to claim 23.

28. (Amended) ~~Use of nucleic acid sequences according to Seq ID Nos. 1-31 and Seq. ID No.52 for expression of polypeptides that can be used as tools~~ A method for finding an active ~~ingredients~~ ingredient against hysteromyoma comprising measuring the

binding of said ingredient to the polypeptide encoded by the nucleic acid comprising SEQ ID NO:16.

29. (Amended) ~~Use of nucleic acid sequences Seq. ID. Nos. 1-31 and Seq. ID No. 52~~ The nucleic acid comprising SEQ ID NO:16 according to claim 28, wherein said sequence is in the sense or antisense form.

30. (Amended) ~~Use of polypeptide partial sequences Seq. ID No. 32 to Seq. ID No. 51 and Seq. ID Nos. 53-55 as pharmaceutical agents in gene therapy for treatment of~~ A method for treating hysteromyoma comprising administering a therapeutically effective amount of a polypeptide comprising SEQ ID NO:38 according to claim 23.

31. (Amended) ~~Use of polypeptide partial sequences Seq. ID No.32 to Seq. ID. No. 51 and Seq. ID Nos. 53-55 for the production of a pharmaceutical agent~~ A method for preparing a pharmaceutical ~~agent~~ composition for ~~treatment of~~ treating hysteromyoma comprising mixing a pharmaceutically acceptable carrier with a polypeptide comprising SEQ ID NO:38 according to claim 23.